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1600

p#12

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/647,340A697
DATE: 07/25/2002
TIME: 08:40:21Input Set : A:\501d4.app
Output Set: N:\CRF3\07252002\I647340A.raw

PCO

P.6

4 <110> APPLICANT: Brunkow, Mary E.
 5 Jeffery, Eric W.
 6 Hjerrild, Kathryn A.
 7 Ramsdell, Fred
 11 <120> TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING THE
 12 MOUSE SCURFY PHENOTYPE AND ITS HUMAN ORTHOLOG
 15 <130> FILE REFERENCE: 240083.501D4
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/647,340A
 18 <141> CURRENT FILING DATE: 2000-10-24
 20 <160> NUMBER OF SEQ ID NOS: 14
 22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2160
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Mus musculus
 29 <400> SEQUENCE: 1

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31	ccagacacag ctctgtggc gaaagtggca gagaggtatt gaggggtgggt gtcaggagcc	120
32	caccagtaca gctggaaaca cccagccact ccagctcccg gcaacttctc ctgactctgc	180
33	cttcagacga gacttggaaag acagtcatct ctcagcagct cctctgcgt tatecagcct	240
34	gcctctgaca agaaccaa at gcccaaccct aggccagcca agcctatggc tccttccttg	300
35	gccttggcc catccccagg agtcttgcca agcttggaga ctgcacccaa gggctcagaa	360
36	cttcttaggaa ccaggggctc tgggggaccc ttccaaaggc gggacctgct aagtggggcc	420
37	cacaccttctt cttccttggaa ccccttgcac ccatcccagc tgcatgtgcc tacagtgc	480
38	ctagtcatgg tggcacccgtc tggggcccgta cttagtccctt caccacccat acaggccctt	540
39	ctccaggaca gaccacactt catgcatacg ctctccactg tggatgcacca tgcccagacc	600
40	cctgtgtctt aagtgcgtcc actggacaac ccagccatga tcagcctccc accacccat	660
41	gctgccactg gggcttctc cctcaaggcc cggcctggcc tgccacctgg gatcaatgtg	720
42	gccagtctgg aatgggtgtc cagggagcca gctctactct gcacccccc acgctgggt	780
43	acaccccgaa aagacagcaa cttttggct gcaccccaag gatcctaccc actgtctggca	840
44	aatggagtct gcaagtggcc tgggtgtgag aaggcttgcg aggagccaga agagtttctc	900
45	aagcactgccc aagcagatca tctcttggat gagaaaggca aggcccagtg cctcccccac	960
46	agagaagtgg tgcatgtctt ggagcagcag ctggagctgg aaaaggagaa gctgggagct	1020
47	atgcaggccc acctggctgg gaagatggcg ctggccagg ctccatctgt ggcctcaatg	1080
48	gacaagagct tttgtgtcat cttgtgtccacc agtactcagg gcagtgtgt cccggcctgg	1140
49	tctgtcttccc gggaggctcc agacggcgcc ctgtttgtcag tgccggaggca cctctgggaa	1200
50	agccatggca atagttccctt cccagagtcc ttccacaca tggactactt caagtaccac	1260
51	aatatgcgac ccccttccac ctatgccacc cttatccgtt gggccatccct ggaagccccg	1320
52	gagaggcaga ggacactcaa taaaatctac cattggtttca ctgcgtt cgcctacttc	1380
53	agaaaccacc cccacccatcg gaagaatggcc atccggcaca acctgagccct gcacaagtgc	1440
54	tttgtgcgag tggagagcga gaaggggacca gtgtggaccg tagatgaatt tgagttcgc	1500
55	aagaagagga gccaacgccc caacaagtgc tccaatccct gcccttgacc tcaaaaccaa	1560
56	gaaaagggtgg gcgggggagg gggccaaaac catgagactg aggctgtggg ggcaaggagg	1620

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57	caagtccat	gtgtacctat	ggaaaccggg	cgtatgtc	cctgctatca	gggcctctgc	1680
58	tccctatcta	gctgcctcc	tagatcatat	catctgcctt	acagctgaga	gggggtccaa	1740
59	tcccaggcta	gccccatgtt	ccaacctagc	cccaagatga	actttccagt	caaagagccc	1800
60	tcacaaccag	ctatacatat	ctgccttggc	cactgccaag	cagaaagatg	acagacacca	1860
61	tcctaattt	tactcaaccc	aaaccctaaa	acatgaagag	cctgccttgg	tacattcg	1920
62	aactttcaaa	gttagtcatg	cagtcacaca	tgactgcagt	cctactgact	cacacccaa	1980
63	agcactcacc	cacaacatct	gaaaccacgg	gcactatcac	acatagggt	atatacagac	2040
64	ccttacacag	caacagcact	gaaaccttca	caattacatc	cccccaaacc	acacaggcat	2100
65	aactgatcat	acgcagcctc	aagcaatgcc	caaaatacaa	gtcagacaca	gcttgtcaga	2160
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68	<211>	LENGTH:	429				
69	<212>	TYPE:	PRT				
70	<213>	ORGANISM:	Mus musculus				
72	<400>	SEQUENCE:	2				
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74	1	5	10	15			
75	Gly Pro Ser Pro Gly Val Leu Pro Ser Trp Lys Thr Ala Pro Lys Gly						
76	20	25	30				
77	Ser Glu Leu Leu Gly Thr Arg Gly Ser Gly Gly Pro Phe Gln Gly Arg						
78	35	40	45				
79	Asp Leu Arg Ser Gly Ala His Thr Ser Ser Leu Asn Pro Leu Pro						
80	50	55	60				
81	Pro Ser Gln Leu Gln Leu Pro Thr Val Pro Leu Val Met Val Ala Pro						
82	65	70	75	80			
83	Ser Gly Ala Arg Leu Gly Pro Ser Pro His Leu Gln Ala Leu Leu Gln						
84	85	90	95				
85	Asp Arg Pro His Phe Met His Gln Leu Ser Thr Val Asp Ala His Ala						
86	100	105	110				
87	Gln Thr Pro Val Leu Gln Val Arg Pro Leu Asp Asn Pro Ala Met Ile						
88	115	120	125				
89	Ser Leu Pro Pro Pro Ser Ala Ala Thr Gly Val Phe Ser Leu Lys Ala						
90	130	135	140				
91	Arg Pro Gly Leu Pro Pro Gly Ile Asn Val Ala Ser Leu Glu Trp Val						
92	145	150	155	160			
93	Ser Arg Glu Pro Ala Leu Leu Cys Thr Phe Pro Arg Ser Gly Thr Pro						
94	165	170	175				
95	Arg Lys Asp Ser Asn Leu Leu Ala Ala Pro Gln Gly Ser Tyr Pro Leu						
96	180	185	190				
97	Leu Ala Asn Gly Val Cys Lys Trp Pro Gly Cys Glu Lys Val Phe Glu						
98	195	200	205				
99	Glu Pro Glu Glu Phe Leu Lys His Cys Gln Ala Asp His Leu Leu Asp						
100	210	215	220				
101	Glu Lys Gly Lys Ala Gln Cys Leu Leu Gln Arg Glu Val Val Gln Ser						
102	225	230	235	240			
103	Leu Glu Gln Gln Leu Glu Leu Glu Lys Glu Lys Leu Gly Ala Met Gln						
104	245	250	255				
105	Ala His Leu Ala Gly Lys Met Ala Leu Ala Lys Ala Pro Ser Val Ala						
106	260	265	270				
107	Ser Met Asp Lys Ser Ser Cys Cys Ile Val Ala Thr Ser Thr Gln Gly						

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108	275	280	285
109	Ser Val Leu Pro Ala Trp Ser Ala Pro Arg Glu Ala Pro Asp Gly Gly		
110	290	295	300
111	Leu Phe Ala Val Arg Arg His Leu Trp Gly Ser His Gly Asn Ser Ser		
112	305	310	315
113	Phe Pro Glu Phe Phe His Asn Met Asp Tyr Phe Lys Tyr His Asn Met		320
114	325/	330	335
115	Arg Pro Pro Phe Thr Tyr Ala Thr Leu Ile Arg Trp Ala Ile Leu Glu		
116	340	345	350
117	Ala Pro Glu Arg Gln Arg Thr Leu Asn Glu Ile Tyr His Trp Phe Thr		
118	355	360	365
119	Arg Met Phe Ala Tyr Phe Arg Asn His Pro Ala Thr Trp Lys Asn Ala		
120	370	375	380
121	Ile Arg His Asn Leu Ser Leu His Lys Cys Phe Val Arg Val Glu Ser		
122	385	390	395
123	Glu Lys Gly Ala Val Trp Thr Val Asp Glu Phe Glu Phe Arg Lys Lys		400
124	405	410	415
125	Arg Ser Gln Arg Pro Asn Lys Cys Ser Asn Pro Cys Pro		
126	420	425	
128	<210> SEQ ID NO: 3		
129	<211> LENGTH: 1869		
130	<212> TYPE: DNA		
131	<213> ORGANISM: Homo sapien		
133	<400> SEQUENCE: 3		
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135	cgtacagcgt ggttttctt ctcggataaa aagcaaagt gttttgata cgtgacagtt	120	
136	tcccacaagc caggctgatc ctttctgtc agtccacttc accaagcctg cccttggaca	180	
137	aggaccgcgt gccccacccc aggcttgca agccctcgcc cccttccttgc gcccttggcc	240	
138	catccccagg agcctcgccc agctggaggg ctgcacccaa agcctcagac ctgtgggggg	300	
139	cccgggccccc aggggaacc ttccagggcc gagatctcg aggcggggcc catgcctcct	360	
140	tttcttcctt gaacccatg ccaccatgc agctgcagct gcccacactg cccctagtc	420	
141	tggggcacc ctccggggca cggctgggcc ctttgcccca cttacaggca ctccctcagg	480	
142	acaggccaca tttcatgcac cagctctcaa cggtggatgc ccacgcccc acccctgtgc	540	
143	tgcaggtgca cccctggag agcccagcca tgatcagct cacaccaccc accacccgcca	600	
144	ctggggctt ctccctcaag gcccggctg gcctcccacc tggatcaac gtggccagcc	660	
145	tggaatgggt gtccaggag cccgcactgc tctgcaccc cccaaatccc agtgcaccca	720	
146	ggaaggacag cacccttcg gctgtcccc agagctcta cccactgtcg gcaaattggtg	780	
147	tctgcaagtg gccccatgt gagaaggct tcgaagagcc agaggacttc ctcaagcact	840	
148	gccaggcgga ccatcttcg gatgagaagg gcagggcaca atgtctctc cagagagaga	900	
149	tggtacagtc tctggagcag cagctggtc tggagaagga gaagctgagt gcatgcagg	960	
150	cccacctggc tggaaaatg gcactgacca aggcttcattc tggatca tccgacaaagg	1020	
151	gtccctgtc catctgtct gctggcagcc aaggccctgt cgtcccaagcc tggatccggcc	1080	
152	cccgggagggcc ccctgacagc ctgttgcgt tcggaggca cctgtgggggt agccatggaa	1140	
153	acagcacatt cccagaggta ctccacaaca tggactactt caagttccac aacatgcac	1200	
154	ccctttcac ctacgccacg ctcatccgt gggccatcc ggaggctcca gagaaggcagc	1260	
155	ggacactcaa tgatctac cactggttca cacgcatgtt tgccttc agaaaccatc	1320	
156	ctgccacctg gaagaacgcc atccgccaca acctgagtct gcacaagtgc tttgtgcggg	1380	
157	tggagagcga gaaggggct gtgtggaccg tggatgagct ggagttccgc aagaaacgga	1440	
158	gccagaggcc cagcagggtgt tccaaaccta cacctggccc ctgacccaa gatcaaggaa	1500	

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159	aggaggatgg	acgaacaggg	gccaactgg	tgggaggcgag	aggtgtgggg	ggcagggatg	1560									
160	ataggccctg	gatgtgccc	caggaccaa	gaagtggaggt	ttccactgtc	ttgcctgcca	1620									
161	gggccccctgt	tcccccgctg	gcagccaccc	cctccccat	cataccctt	gcuccaaggc	1680									
162	tgctcagagg	ggcccccgtc	ctggcccccag	cccccaccc	cgcggccagac	acacccccc	1740									
163	gtcgagccct	gcagccaaac	agagccttca	caaccagcca	cacagagcct	gcctcagctg	1800									
164	ctcgacaga	ttacttcagg	gctggaaaag	tcacacagac	acacaaaatg	tcacaatcct	1860									
165	gtccctcac						1869									
167	<210>	SEQ ID NO:	4													
168	<211>	LENGTH:	431													
169	<212>	TYPE:	PRT													
170	<213>	ORGANISM:	Homo sapien													
172	<400>	SEQUENCE:	4													
173	Met	Pro	Asn	Pro	Arg	Pro	Gly	Lys	Pro	Ser	Ala	Pro	Ser	Leu	Ala	Leu
174	1								10							15
175	Gly	Pro	Ser	Pro	Gly	Ala	Ser	Pro	Ser	Trp	Arg	Ala	Ala	Pro	Lys	Ala
176									20							30
177	Ser	Asp	Leu	Leu	Gly	Ala	Arg	Gly	Pro	Gly	Gly	Thr	Phe	Gln	Gly	Arg
178									35							45
179	Asp	Leu	Arg	Gly	Gly	Ala	His	Ala	Ser	Ser	Ser	Ser	Leu	Asn	Pro	Met
180									50							60
181	Pro	Pro	Ser	Gln	Leu	Gln	Leu	Pro	Thr	Leu	Pro	Leu	Val	Met	Val	Ala
182									65							80
183	Pro	Ser	Gly	Ala	Arg	Leu	Gly	Pro	Leu	Pro	His	Leu	Gln	Ala	Leu	Leu
184									85							95
185	Gln	Asp	Arg	Pro	His	Phe	Met	His	Gln	Leu	Ser	Thr	Val	Asp	Ala	His
186									100							110
187	Ala	Arg	Thr	Pro	Val	Leu	Gln	Val	His	Pro	Leu	Glu	Ser	Pro	Ala	Met
188									115							125
189	Ile	Ser	Leu	Thr	Pro	Pro	Thr	Thr	Ala	Thr	Gly	Val	Phe	Ser	Leu	Lys
190									130							140
191	Ala	Arg	Pro	Gly	Leu	Pro	Pro	Gly	Ile	Asn	Val	Ala	Ser	Leu	Glu	Trp
192									145							160
193	Val	Ser	Arg	Glu	Pro	Ala	Leu	Leu	Cys	Thr	Phe	Pro	Asn	Pro	Ser	Ala
194									165							175
195	Pro	Arg	Lys	Asp	Ser	Thr	Leu	Ser	Ala	Val	Pro	Gln	Ser	Ser	Tyr	Pro
196									180							190
197	Leu	Leu	Ala	Asn	Gly	Val	Cys	Lys	Trp	Pro	Gly	Cys	Glu	Lys	Val	Phe
198									195							205
199	Glu	Glu	Pro	Glu	Asp	Phe	Leu	Lys	His	Cys	Gln	Ala	Asp	His	Leu	Leu
200									210							220
201	Asp	Glu	Lys	Gly	Arg	Ala	Gln	Cys	Leu	Leu	Gln	Arg	Glu	Met	Val	Gln
202									225							240
203	Ser	Leu	Glu	Gln	Gln	Leu	Val	Leu	Glu	Lys	Glu	Lys	Leu	Ser	Ala	Met
204									245							255
205	Gln	Ala	His	Leu	Ala	Gly	Lys	Met	Ala	Leu	Thr	Lys	Ala	Ser	Ser	Val
206									260							270
207	Ala	Ser	Ser	Asp	Lys	Gly	Ser	Cys	Cys	Ile	Val	Ala	Ala	Gly	Ser	Gln
208									275							285
209	Gly	Pro	Val	Val	Pro	Ala	Trp	Ser	Gly	Pro	Arg	Glu	Ala	Pro	Asp	Ser

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210	290	295	300	
211	Leu Phe Ala Val Arg Arg His Leu Trp Gly Ser His Gly Asn Ser Thr			
212	305	310	315	320
213	Phe Pro Glu Phe Leu His Asn Met Asp Tyr Phe Lys Phe His Asn Met			
214	325	330	335	
215	Arg Pro Pro Phe Thr Tyr Ala Thr Leu Ile Arg Trp Ala Ile Leu Glu			
216	340	345	350	
217	Ala Pro Glu Lys Gln Arg Thr Leu Asn Glu Ile Tyr His Trp Phe Thr			
218	355	360	365	
219	Arg Met Phe Ala Phe Phe Arg Asn His Pro Ala Thr Trp Lys Asn Ala			
220	370	375	380	
221	Ile Arg His Asn Leu Ser Leu His Lys Cys Phe Val Arg Val Glu Ser			
222	385	390	395	400
223	Glu Lys Gly Ala Val Trp Thr Val Asp Glu Leu Glu Phe Arg Lys Lys			
224	405	410	415	
225	Arg Ser Gln Arg Pro Ser Arg Cys Ser Asn Pro Thr Pro Gly Pro			
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229	<211> LENGTH: 23			
230	<212> TYPE: DNA			
231	<213> ORGANISM: Artificial Sequence			
233	<220> FEATURE:			
234	<223> OTHER INFORMATION: Primer for generation of mouse Fkh cDNA			
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239	<210> SEQ ID NO: 6			
240	<211> LENGTH: 23			
241	<212> TYPE: DNA			
242	<213> ORGANISM: Artificial Sequence			
244	<220> FEATURE:			
245	<223> OTHER INFORMATION: Primer for generation of mouse Fkh cDNA			
247	<400> SEQUENCE: 6			
248	gcagatctga caagctgtgt ctg			23
250	<210> SEQ ID NO: 7			
251	<211> LENGTH: 21			
252	<212> TYPE: DNA			
253	<213> ORGANISM: Artificial Sequence			
255	<220> FEATURE:			
256	<223> OTHER INFORMATION: Primer for generation of human Fkh cDNA			
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261	<210> SEQ ID NO: 8			
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263	<212> TYPE: DNA			
264	<213> ORGANISM: Artificial Sequence			
266	<220> FEATURE:			
267	<223> OTHER INFORMATION: Primer for generation of human Fkh cDNA			
269	<400> SEQUENCE: 8			
270	gcaagacagt ggaaacctca c			21

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 3,6,9,12,15
Seq#:14; N Pos. 1,7,10,13,16,19